# Module 7: Introduction to Gibbs Sampling

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#### Intoduction

In this lab, we will derive conditional distributions, code a Gibbs sampler, and analyze the output of the Gibbs sampler.

Consider the following Exponential model for observation(s)  $x_{1:n} = (x_1, \dots, x_n)^{1:n}$ :

$$p(x|a,b) = ab \exp(-abx) \mathbf{1}_{x>0},$$

where the  $x_i$  are assumed to be iid for i = 1, ... n. and suppose the prior is

$$p(a,b) = \exp(-a-b)\mathbf{1}_{a,b>0}.$$

We want to sample from the posterior  $p(a, b|x_{1:n})$ .

Tasks

- 1. Find the conditional distributions needed for implementing a Gibbs sampler.
- 2. Code up our own Gibbs sampler using part (1).
- 3. Run the Gibbs sampler, providing convergence diagnostics.
- 4. Plot a histogram or a density estimate of the estimated posterior using (2) and (3).
- 5. How do you know that your estimated posterior in (3) is reliable?

#### Task 1: Conditional distributions

Consider the following Exponential model for observation(s)  $x_{1:n} = (x_1, \ldots, x_n)$ :

$$p(x|a,b) = ab \exp(-abx) \mathbf{1}_{x>0}$$

and suppose the prior is

$$p(a,b) = \exp(-a-b)\mathbf{1}_{a,b>0}.$$

Our final goal is to sample from the posterior p(a, b|x).

$$p(\boldsymbol{x}|a,b) = \prod_{i=1}^{n} p(x_i|a,b)$$
$$= \prod_{i=1}^{n} ab \exp(-abx_i)$$
$$= (ab)^n \exp\left(-ab\sum_{i=1}^{n} x_i\right).$$

<sup>&</sup>lt;sup>1</sup>Please note that in the attached data there are 30 observations, which can be found in data-exponential.csv.

The function is symmetric for a and b, so we only need to derive  $p(a|\mathbf{x},b)$ . This conditional distribution satisfies

$$p(a|\mathbf{x},b) \propto_a p(a,b,\mathbf{x})$$

$$= p(\mathbf{x}|a,b)p(a,b)$$

$$= (ab)^n \exp\left(-ab\sum_{i=1}^n x_i\right) \times \exp(-a-b)I(a,b>0)$$

$$\propto a^n \exp(-abn\bar{x}-a)\mathbf{1}_{a>0}$$

$$= a^{n+1-1} \exp(-(bn\bar{x}+1)a)\mathbf{1}_{a>0}$$

$$\propto \operatorname{Ga}(a|n+1,bn\bar{x}+1).$$

Therefore,  $p(a|b,x) = Ga(a|n+1, bn\bar{x}+1)$  and by symmetry,  $p(b|a,x) = Ga(b|n+1, an\bar{x}+1)$ .

We now load the packages we need and the observed data X.

```
library(coda)
library(ggplot2)
X=c(
0.0371331907051745,0.271390503356533,2.40473359881563,
0.279129389456793,3.89335288168723,6.07299593757399,
2.0008345204379,0.374140078068601,0.269576448538397,
1.316028759158,2.42209106222679,1.12711988643488,
0.847399458693192,0.0916006407183253,3.15166571883227,
0.122355493965856,1.6631530013599,2.31930895969008,
0.254301124443481,2.91553389072551,1.99536939381821,
2.46937213527566,9.4394789881428,5.27195433646316,
0.45310761063482,1.65998358370856,2.95869986327957,
2.82643679251663,0.407467252515871,1.07017463071046
)
```

## Task 2: Gibbs sampling code

Here the pseudo-code

And here the code

```
sampleGibbs=function(a0, b0, S, X){
  # get sum, which is sufficient statistic
  x=sum(X)
  # qet n
 n=length(X)
  # create empty matrix, allocate memory for efficiency
 AB=matrix(NA, nrow=S, ncol=2)
  # iterate the algorithm
 a=a0;b=b0
  for(j in 1:S){ # number of iteration
   AB[j,1]=a
   AB[j,2]=b
   a=rgamma(1,shape=n+1, rate=b*x+1)
   b=rgamma(1,shape=n+1, rate=a*x+1)
 }
 return(AB)
```

### Task 3: Run the Gibbs sampler

We start with some arbitrary initial values  $a_0 = b_0 = 1$ .

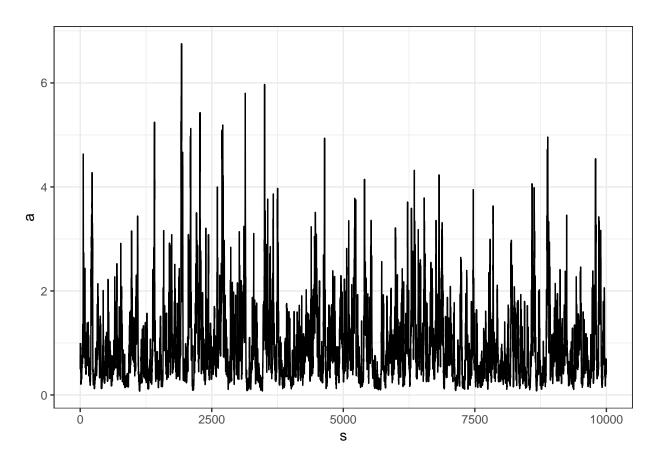
```
# run Gibbs sampler
a0=b0=1 # initial values = 1
S=10000
AB=sampleGibbs(a0 , b0 , S , X)
head(AB)

## [,1] [,2]
## [1,] 1.0000000 1.0000000
## [2,] 0.5092957 0.8105875
## [3,] 0.6787493 0.6567587
## [4,] 0.7442373 0.5887998
## [5,] 0.7659561 0.8472438
## [6,] 0.5198861 1.1419555

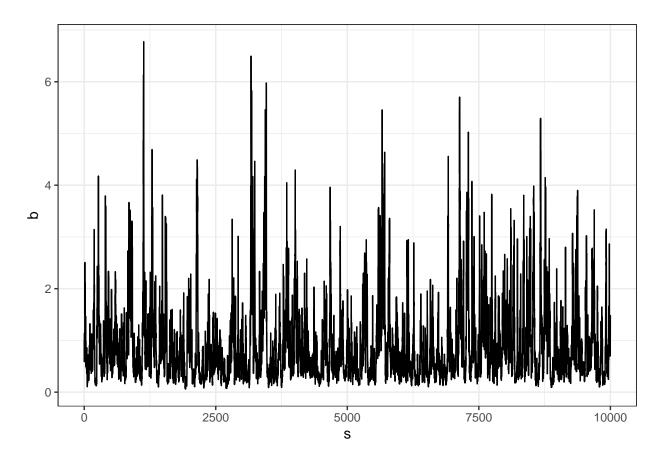
df=data.frame(s=1:S, a=AB[,1], b=AB[,2])
```

We now want to assess the convergence of the algorithm, so we use a traceplot

```
ggplot(df)+
  geom_line(aes(x=s, y=a))+
  theme_bw()
```



```
ggplot(df)+
geom_line(aes(x=s, y=b))+
theme_bw()
```



Let's also look at the Effective Sample Size ratio computing using the package coda.

```
effectiveSize(AB[,1])/S*100
```

```
## var1
## 3.752515
```

### effectiveSize(AB[,2])/S\*100

```
## var1
## 3.64166
```

This is quite low, and indeed, even from the traceplots we can see some **autocorrelation** (that is some local trend in the traces). [**Remark:** This is because the samples are too close to one another and are very likely to be correlated.]

A way to increase the ESS ratio, is trough thinning. That is the process of considering only samples at a certain distance from each other

```
# AB is the original dataframe
# ABthinned is the thinned version
ABthinned=AB[seq(1,S,by=25),]
Sthinned=dim(ABthinned)[1]
print(Sthinned)
```

```
## [1] 400
```

```
effectiveSize(ABthinned[,1])/Sthinned*100

## var1
## 80.33565

effectiveSize(ABthinned[,2])/Sthinned*100

## var1
## 86.90805
```

In this case we have increased the informativity of our sample but we have also reduced its size. In a sense we have *compressed our sample*, because the ESS of both the original samples nd the thinned version is similar even though we have a tenfold reduction in size.

```
c(effectiveSize(ABthinned[,1]),effectiveSize(AB[,1]))

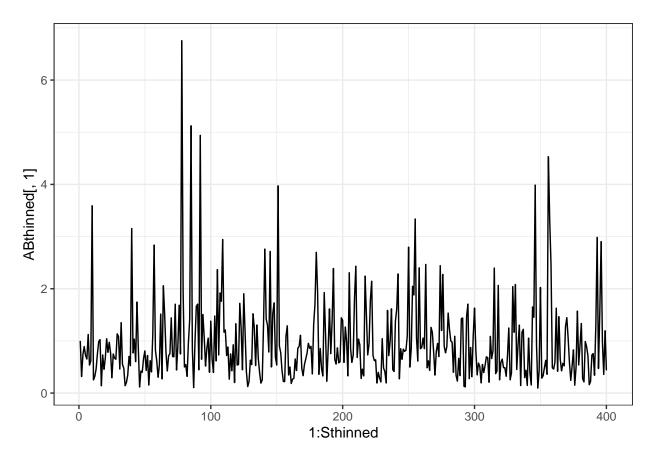
## var1 var1
## 321.3426 375.2515

c(effectiveSize(ABthinned[,2]),effectiveSize(AB[,2]))

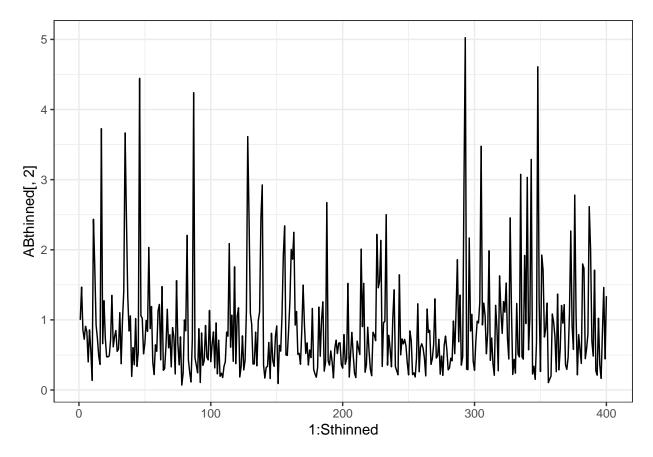
## var1 var1
## 347.6322 364.1660

Let's plot the traces of the thinned sample
```

```
ggplot()+
  geom_line(aes(x=1:Sthinned, y=ABthinned[,1]))+
  theme_bw()
```



```
ggplot()+
geom_line(aes(x=1:Sthinned, y=ABthinned[,2]))+
theme_bw()
```



These plots seems to indicate convergence to a stationary distribution. And though thinning we have manage to eliminate most of the correlation.

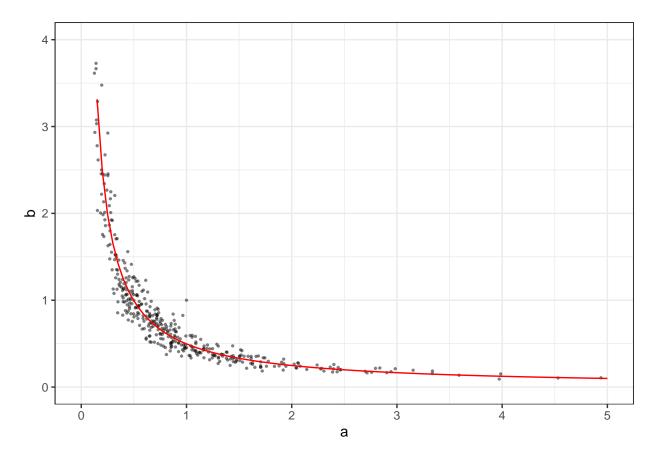
### Task 4

Plot a histogram or a density estimate of the estimated posterior using tasks (2) and (3).

```
prod=mean(ABthinned[,1]*ABthinned[,2]) # mean of a*b
f=function(x){return(prod/x)}
dft=data.frame(a=ABthinned[,1],b=ABthinned[,2])
```

```
ggplot(dft, aes(x = a, y = b)) +
    #geom_density_2d(aes(color = ..level..),bins=10)+
    geom_point(alpha=0.5,size=0.5)+
    xlim(0,5)+ylim(0,4)+
    geom_function(fun=f,color="red")+
    theme_bw()
```

## Warning: Removed 6 rows containing missing values ('geom\_point()').

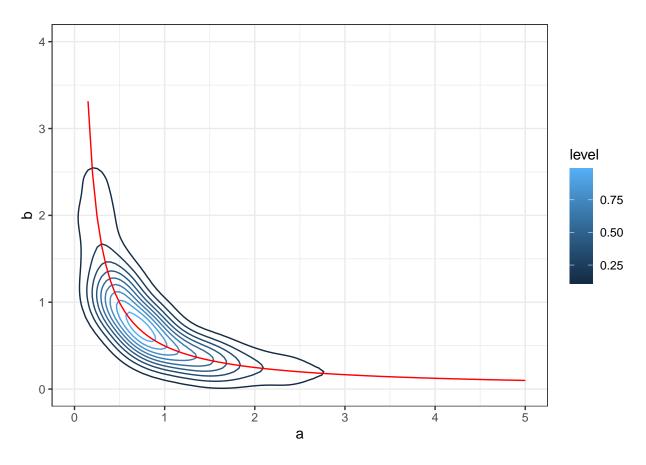


Plot the distribution density of a and b (higher density when a and b are similar and lower density when a and b are far from each other)

```
ggplot(dft, aes(x = a, y = b)) +
  geom_density_2d(aes(color = ..level..),bins=10)+
  #geom_point(alpha=0.1,size=0.5)+
  xlim(0,5)+ylim(0,4)+
  geom_function(fun=f,color="red")+
  theme_bw()
```

```
## Warning: The dot-dot notation ('..level..') was deprecated in ggplot2 3.4.0.
## i Please use 'after_stat(level)' instead.
```

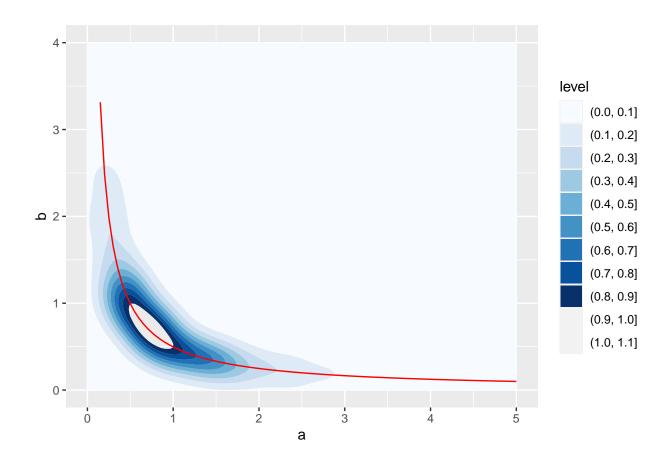
## Warning: Removed 6 rows containing non-finite values ('stat\_density2d()').



```
ggplot(dft, aes(x = a, y = b)) +
geom_density_2d_filled() +
scale_fill_brewer()+
xlim(0,5)+ylim(0,4)+
geom_function(fun=f,color="red")
```

## Warning: Removed 6 rows containing non-finite values
## ('stat\_density2d\_filled()').

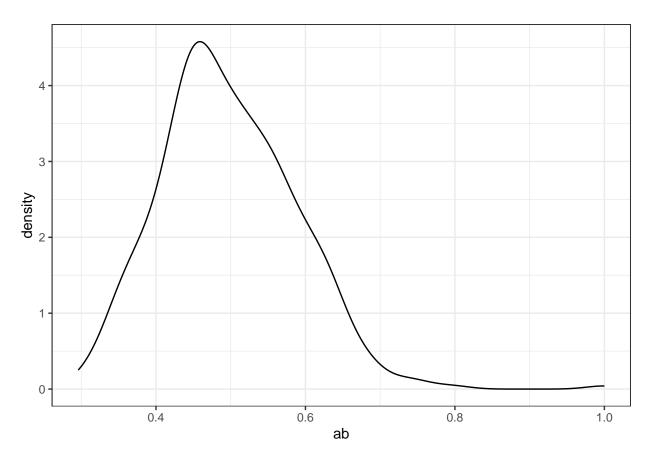
## Warning in RColorBrewer::brewer.pal(n, pal): n too large, allowed maximum for palette Blues is 9
## Returning the palette you asked for with that many colors



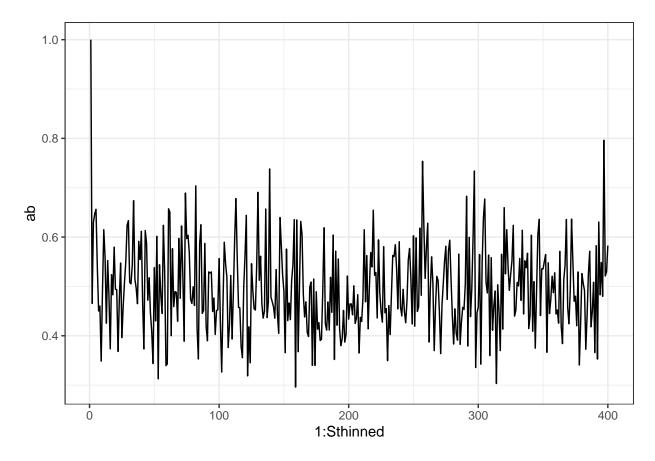
# Task 5

Why am I plotting this thin red line?

```
# the distribution of a*b
ab=ABthinned[,1]*ABthinned[,2]
ggplot()+
  geom_density(aes(x=ab))+
  theme_bw()
```



```
ggplot()+
  geom_line(aes(x=1:Sthinned, y=ab))+
  theme_bw()
```



From these plots it seems that ab can be estimated much more easily than a and b. Why is that? (**Identifiability**)

### Q: How do you know that your estimated posterior in task (3) is reliable?

A: The density of a and b are very similar, so they have symmetric posterior density, which verifies our assumption before.